



tcg atg aag cct atc aat gaa gac ttg gat gag ggc atc atg gtg gtc		384
Ser Met Lys Pro Ile Asn Glu Asp Leu Asp Glu Gly Ile Met Val Val		
115	120	125
tac aag cgc aac atc gtg gcg cac acc ttt aag gta cggt gtc tac caa		432
Tyr Lys Arg Asn Ile Val Ala His Thr Phe Lys Val Arg Val Tyr Gln		
130	135	140
aag gtt ttg acg ttt cgt cgt agc tac gct tac atc tac acc act tat		480
Lys Val Leu Thr Phe Arg Arg Ser Tyr Ala Tyr Ile Tyr Thr Thr Tyr		
145	150	155
ctg ctg ggc agc aat acg gaa tac gtg gcg cct cct atg tgg gag att		528
Leu Leu Gly Ser Asn Thr Glu Tyr Val Ala Pro Pro Met Trp Glu Ile		
165	170	175
cat cac atc aac aag ttt gct caa tgc tac agt tcc tac agc cgc gtt		576
His His Ile Asn Lys Phe Ala Gln Cys Tyr Ser Ser Tyr Ser Arg Val		
180	185	190
ata gga ggc acg gtt ttc gtg gca tat cat agg gac agt tat gaa aac		624
Ile Gly Gly Thr Val Phe Val Ala Tyr His Arg Asp Ser Tyr Glu Asn		
195	200	205
aaa acc atg caa tta att ccc gac gat tat tcc aac acc cac agt acc		672
Lys Thr Met Gln Leu Ile Pro Asp Asp Tyr Ser Asn Thr His Ser Thr		
210	215	220
cgt tac gtg acg gtc aag gat cag tgg cac agc cgc ggc agc acc tgg		720
Arg Tyr Val Thr Val Lys Asp Gln Trp His Ser Arg Gly Ser Thr Trp		
225	230	235
ctc tat cgt gag acc tgt aat ctg aac tgt atg ctg acc atc act act		768
Leu Tyr Arg Glu Thr Cys Asn Leu Asn Cys Met Leu Thr Ile Thr Thr		
245	250	255
gcg cgc tcc aag tat cct tat cat ttt ttt gca act tcc acg ggt gat		816
Ala Arg Ser Lys Tyr Pro Tyr His Phe Phe Ala Thr Ser Thr Gly Asp		
260	265	270
gtg gtt tac att tct cct ttc tac aac gga acc aat cgc aat gcc agc		864
Val Val Tyr Ile Ser Pro Phe Tyr Asn Gly Thr Asn Arg Asn Ala Ser		
275	280	285
tac ttt gga gaa aac gcc gac aag ttt ttc att ttc ccg aac tac acc		912
Tyr Phe Gly Glu Asn Ala Asp Lys Phe Phe Ile Phe Pro Asn Tyr Thr		
290	295	300
atc gtt tcc gac ttt gga aga ccc aac gct gcg cca gaa acc cat agg		960
Ile Val Ser Asp Phe Gly Arg Pro Asn Ala Ala Pro Glu Thr His Arg		
305	310	315
ttg gtg gct ttt ctc gaa cgt gcc gac tcg gtg atc tct tgg gat ata		1008
Leu Val Ala Phe Leu Glu Arg Ala Asp Ser Val Ile Ser Trp Asp Ile		
325	330	335

cag gac gag aag aat gtc acc tgc cag ctc acc ttc tgg gaa gcc tcg Gln Asp Glu Lys Asn Val Thr Cys Gln Leu Thr Phe Trp Glu Ala Ser 340 345 350	1056
gaa cgt act atc cgt tcc gaa gcc gaa gac tcg tac cac ttt tct tct Glu Arg Thr Ile Arg Ser Glu Ala Glu Asp Ser Tyr His Phe Ser Ser 355 360 365	1104
gcc aaa atg act gca act ttt ctg tct aag aaa caa gaa gtg aac atg Ala Lys Met Thr Ala Thr Phe Leu Ser Lys Lys Gln Glu Val Asn Met 370 375 380	1152
tcc gac tcc gcg ctg gac tgc gta cgt gat gag gct ata aat aag tta Ser Asp Ser Ala Leu Asp Cys Val Arg Asp Glu Ala Ile Asn Lys Leu 385 390 395 400	1200
cag cag att ttc aat act tca tac aat caa aca tat gaa aaa tac gga Gln Gln Ile Phe Asn Thr Ser Tyr Asn Gln Thr Tyr Glu Lys Tyr Gly 405 410 415	1248
aac gtg tcc gtc ttc gaa acc agc ggc ggt ctg gtg gtg ttc tgg caa Asn Val Ser Val Phe Glu Thr Ser Gly Gly Leu Val Val Phe Trp Gln 420 425 430	1296
ggc atc aag caa aaa tct ttg gtg gaa ttg gaa cgt ttg gcc aat cga Gly Ile Lys Gln Lys Ser Leu Val Glu Leu Glu Arg Leu Ala Asn Arg 435 440 445	1344
tcc agt ctg aat atc act cat agg acc aga aga agt acg agt gac aat Ser Ser Leu Asn Ile Thr His Arg Thr Arg Arg Ser Thr Ser Asp Asn 450 455 460	1392
aat aca act cat ttg tcc agc atg gaa tcg gtg cac aat ctg gtc tac Asn Thr Thr His Leu Ser Ser Met Glu Ser Val His Asn Leu Val Tyr 465 470 475 480	1440
gcc cag ctg cag ttc acc tat gac acg ttg cgc ggt tac atc aac cgg Ala Gln Leu Gln Phe Thr Tyr Asp Thr Leu Arg Gly Tyr Ile Asn Arg 485 490 495	1488
gcg ctg gcg caa atc gca gaa gcc tgg tgt gtg gat caa cgg cgc acc Ala Leu Ala Gln Ile Ala Glu Ala Trp Cys Val Asp Gln Arg Arg Thr 500 505 510	1536
cta gag gtc ttc aag gaa ctc agc aag atc aac ccg tca gcc att ctc Leu Glu Val Phe Lys Glu Leu Ser Lys Ile Asn Pro Ser Ala Ile Leu 515 520 525	1584
tcg gcc att tac aac aaa ccg att gcc gcg cgt ttc atg ggt gat gtc Ser Ala Ile Tyr Asn Lys Pro Ile Ala Ala Arg Phe Met Gly Asp Val 530 535 540	1632
ttg ggc ctg gcc agc tgc gtg acc atc aac caa acc acc agc gtc aag gtg Leu Gly Leu Ala Ser Cys Val Thr Ile Asn Gln Thr Ser Val Lys Val 545 550 555 560	1680
ctg cgt gat atg aac gtg aag gaa tcg cca gga cgc tgc tac tca cga	1728

Leu Arg Asp Met Asn Val Lys Glu Ser Pro Gly Arg Cys Tyr Ser Arg		
565	570	575
ccc gtg gtc atc ttt aat ttc gcc aac agc tcg tac gtg cag tac ggt		1776
Pro Val Val Ile Phe Asn Phe Ala Asn Ser Ser Tyr Val Gln Tyr Gly		
580	585	590
caa ctg ggc gag gac aac gaa atc ctg ttg ggc aac cac cgc act gag		1824
Gln Leu Gly Glu Asp Asn Glu Ile Leu Leu Gly Asn His Arg Thr Glu		
595	600	605
gaa tgt cag ctt ccc agc ctc aag atc ttc atc gcc ggg aac tcg gcc		1872
Glu Cys Gln Leu Pro Ser Leu Lys Ile Phe Ile Ala Gly Asn Ser Ala		
610	615	620
tac gag tac gtg gac tac ctc ttc aaa cgc atg att gac ctc agc agt		1920
Tyr Glu Tyr Val Asp Tyr Leu Phe Lys Arg Met Ile Asp Leu Ser Ser		
625	630	635
640		
atc tcc acc gtc gac agc atg atc gcc ctg gat atc gac ccg ctg gaa		1968
Ile Ser Thr Val Asp Ser Met Ile Ala Leu Asp Ile Asp Pro Leu Glu		
645	650	655
aat acc gac ttc agg gta ctg gaa ctt tac tcg cag aaa gag ctg cgt		2016
Asn Thr Asp Phe Arg Val Leu Glu Leu Tyr Ser Gln Lys Glu Leu Arg		
660	665	670
tcc agc aac gtt ttt gac ctc gaa gag atc atg cgc gaa ttc aac tcg		2064
Ser Ser Asn Val Phe Asp Leu Glu Glu Ile Met Arg Glu Phe Asn Ser		
675	680	685
tac aag cag cgg gta aag tac gtg gag gac aag gta gtc gac ccg cta		2112
Tyr Lys Gln Arg Val Lys Tyr Val Glu Asp Lys Val Val Asp Pro Leu		
690	695	700
ccg ccc tac ctc aag ggt ctg gac gac ctc atg agc ggc ctg ggc gcc		2160
Pro Pro Tyr Leu Lys Gly Leu Asp Asp Leu Met Ser Gly Leu Gly Ala		
705	710	715
720		
gcg gga aag gcc gtt ggc gta gcc att ggg gcc gtg ggt ggc gcg gtg		2208
Ala Gly Lys Ala Val Gly Val Ala Ile Gly Ala Val Gly Gly Ala Val		
725	730	735
gcc tcc gtg gtc gaa ggc gtt gcc acc ttc ctc aaa aac ccc ttc gga		2256
Ala Ser Val Val Glu Gly Val Ala Thr Phe Leu Lys Asn Pro Phe Gly		
740	745	750
755		
gcc ttc acc atc atc ctc gtg gcc ata gcc gta gtc att atc act tat		2304
Ala Phe Thr Ile Ile Leu Val Ala Ile Ala Val Val Ile Ile Thr Tyr		
760	765	
ttg atc tat act cga cag cgg cgt ctg tgc acg cag ccg ctg cag aac		2352
Leu Ile Tyr Thr Arg Gln Arg Arg Leu Cys Thr Gln Pro Leu Gln Asn		
770	775	780
ctc ttt ccc tat ctg gtg tcc gcc gac ggg acc acc gtg acg tcg ggc		2400
Leu Phe Pro Tyr Leu Val Ser Ala Asp Gly Thr Thr Val Thr Ser Gly		

785	790	795	800	
agc acc aaa gac acg tcg tta cag gct ccg cct tcc tac gag gaa agt				2448
Ser Thr Lys Asp Thr Ser Leu Gln Ala Pro Pro Ser Tyr Glu Glu Ser				
805	810	815		
gtt tat aat tct ggt cgc aaa gga ccg gga cca ccg tcg tct gat gca				2496
Val Tyr Asn Ser Gly Arg Lys Gly Pro Gly Pro Pro Ser Ser Asp Ala				
820	825	830		
tcc acg gcg gct ccg cct tac acc aac gag cag gct tac cag atg ctt				2544
Ser Thr Ala Ala Pro Pro Tyr Thr Asn Glu Gln Ala Tyr Gln Met Leu				
835	840	845		
ctg gcc ctg gcc cgt ctg gac gca gag cag cga gcg cag cag aac ggt				2592
Leu Ala Leu Ala Arg Leu Asp Ala Glu Gln Arg Ala Gln Gln Asn Gly				
850	855	860		
aca gat tct ttg gac gga cag act ggc acg cag gac aag gga cag aag				2640
Thr Asp Ser Leu Asp Gly Gln Thr Gly Thr Gln Asp Lys Gly Gln Lys				
865	870	875	880	
cct aac ctg cta gac cgg ctg cga cat cgc aaa aac ggc tac aga cac				2688
Pro Asn Leu Leu Asp Arg Leu Arg His Arg Lys Asn Gly Tyr Arg His				
885	890	895		
ttg aaa gac tcc gac gaa gaa gag aac gtc tga				2721
Leu Lys Asp Ser Asp Glu Glu Asn Val				
900	905			

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 <212> PRT  
 <213> Human cytomegalovirus

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 20 25 30  
 Ser Ser Thr His Asn Gly Ser His Thr Ser Arg Thr Thr Ser Ala Gln  
 35 40 45  
 Thr Arg Ser Val Tyr Ser Gln His Val Thr Ser Ser Glu Ala Val Ser  
 50 55 60  
 His Arg Ala Asn Glu Thr Ile Tyr Asn Thr Thr Leu Lys Tyr Gly Asp  
 65 70 75 80  
 Val Val Gly Val Asn Thr Thr Lys Tyr Pro Tyr Arg Val Cys Ser Met  
 85 90 95  
 Ala Gln Gly Thr Asp Leu Ile Arg Phe Glu Arg Asn Ile Ile Cys Thr  
 100 105 110  
 Ser Met Lys Pro Ile Asn Glu Asp Leu Asp Glu Gly Ile Met Val Val  
 115 120 125  
 Tyr Lys Arg Asn Ile Val Ala His Thr Phe Lys Val Arg Val Tyr Gln  
 130 135 140  
 Lys Val Leu Thr Phe Arg Arg Ser Tyr Ala Tyr Ile Tyr Thr Thr Tyr  
 145 150 155 160

Leu Leu Gly Ser Asn Thr Glu Tyr Val Ala Pro Pro Met Trp Glu Ile  
 165 170 175  
 His His Ile Asn Lys Phe Ala Gln Cys Tyr Ser Ser Tyr Ser Arg Val  
 180 185 190  
 Ile Gly Gly Thr Val Phe Val Ala Tyr His Arg Asp Ser Tyr Glu Asn  
 195 200 205  
 Lys Thr Met Gln Leu Ile Pro Asp Asp Tyr Ser Asn Thr His Ser Thr  
 210 215 220  
 Arg Tyr Val Thr Val Lys Asp Gln Trp His Ser Arg Gly Ser Thr Trp  
 225 230 235 240  
 Leu Tyr Arg Glu Thr Cys Asn Leu Asn Cys Met Leu Thr Ile Thr Thr  
 245 250 255  
 Ala Arg Ser Lys Tyr Pro Tyr His Phe Phe Ala Thr Ser Thr Gly Asp  
 260 265 270  
 Val Val Tyr Ile Ser Pro Phe Tyr Asn Gly Thr Asn Arg Asn Ala Ser  
 275 280 285  
 Tyr Phe Gly Glu Asn Ala Asp Lys Phe Phe Ile Phe Pro Asn Tyr Thr  
 290 295 300  
 Ile Val Ser Asp Phe Gly Arg Pro Asn Ala Ala Pro Glu Thr His Arg  
 305 310 315 320  
 Leu Val Ala Phe Leu Glu Arg Ala Asp Ser Val Ile Ser Trp Asp Ile  
 325 330 335  
 Gln Asp Glu Lys Asn Val Thr Cys Gln Leu Thr Phe Trp Glu Ala Ser  
 340 345 350  
 Glu Arg Thr Ile Arg Ser Glu Ala Glu Asp Ser Tyr His Phe Ser Ser  
 355 360 365  
 Ala Lys Met Thr Ala Thr Phe Leu Ser Lys Lys Gln Glu Val Asn Met  
 370 375 380  
 Ser Asp Ser Ala Leu Asp Cys Val Arg Asp Glu Ala Ile Asn Lys Leu  
 385 390 395 400  
 Gln Gln Ile Phe Asn Thr Ser Tyr Asn Gln Thr Tyr Glu Lys Tyr Gly  
 405 410 415  
 Asn Val Ser Val Phe Glu Thr Ser Gly Gly Leu Val Val Phe Trp Gln  
 420 425 430  
 Gly Ile Lys Gln Lys Ser Leu Val Glu Leu Glu Arg Leu Ala Asn Arg  
 435 440 445  
 Ser Ser Leu Asn Ile Thr His Arg Thr Arg Arg Ser Thr Ser Asp Asn  
 450 455 460  
 Asn Thr Thr His Leu Ser Ser Met Glu Ser Val His Asn Leu Val Tyr  
 465 470 475 480  
 Ala Gln Leu Gln Phe Thr Tyr Asp Thr Leu Arg Gly Tyr Ile Asn Arg  
 485 490 495  
 Ala Leu Ala Gln Ile Ala Glu Ala Trp Cys Val Asp Gln Arg Arg Thr  
 500 505 510  
 Leu Glu Val Phe Lys Glu Leu Ser Lys Ile Asn Pro Ser Ala Ile Leu  
 515 520 525  
 Ser Ala Ile Tyr Asn Lys Pro Ile Ala Ala Arg Phe Met Gly Asp Val  
 530 535 540  
 Leu Gly Leu Ala Ser Cys Val Thr Ile Asn Gln Thr Ser Val Lys Val  
 545 550 555 560  
 Leu Arg Asp Met Asn Val Lys Glu Ser Pro Gly Arg Cys Tyr Ser Arg  
 565 570 575  
 Pro Val Val Ile Phe Asn Phe Ala Asn Ser Ser Tyr Val Gln Tyr Gly  
 580 585 590  
 Gln Leu Gly Glu Asp Asn Glu Ile Leu Leu Gly Asn His Arg Thr Glu  
 595 600 605  
 Glu Cys Gln Leu Pro Ser Leu Lys Ile Phe Ile Ala Gly Asn Ser Ala

610	615	620	
Tyr Glu Tyr Val Asp Tyr	Leu Phe Lys Arg Met Ile Asp Leu Ser Ser		
625	630	635	640
Ile Ser Thr Val Asp Ser Met Ile Ala Leu Asp Ile Asp Pro Leu Glu			
645	650	655	
Asn Thr Asp Phe Arg Val Leu Glu Leu Tyr Ser Gln Lys Glu Leu Arg			
660	665	670	
Ser Ser Asn Val Phe Asp Leu Glu Glu Ile Met Arg Glu Phe Asn Ser			
675	680	685	
Tyr Lys Gln Arg Val Lys Tyr Val Glu Asp Lys Val Val Asp Pro Leu			
690	695	700	
Pro Pro Tyr Leu Lys Gly Leu Asp Asp Leu Met Ser Gly Leu Gly Ala			
705	710	715	720
Ala Gly Lys Ala Val Gly Val Ala Ile Gly Ala Val Gly Gly Ala Val			
725	730	735	
Ala Ser Val Val Glu Gly Val Ala Thr Phe Leu Lys Asn Pro Phe Gly			
740	745	750	
Ala Phe Thr Ile Ile Leu Val Ala Ile Ala Val Val Ile Ile Thr Tyr			
755	760	765	
Leu Ile Tyr Thr Arg Gln Arg Arg Leu Cys Thr Gln Pro Leu Gln Asn			
770	775	780	
Leu Phe Pro Tyr Leu Val Ser Ala Asp Gly Thr Thr Val Thr Ser Gly			
785	790	795	800
Ser Thr Lys Asp Thr Ser Leu Gln Ala Pro Pro Ser Tyr Glu Glu Ser			
805	810	815	
Val Tyr Asn Ser Gly Arg Lys Gly Pro Gly Pro Pro Ser Ser Asp Ala			
820	825	830	
Ser Thr Ala Ala Pro Pro Tyr Thr Asn Glu Gln Ala Tyr Gln Met Leu			
835	840	845	
Leu Ala Leu Ala Arg Leu Asp Ala Glu Gln Arg Ala Gln Gln Asn Gly			
850	855	860	
Thr Asp Ser Leu Asp Gly Gln Thr Gly Thr Gln Asp Lys Gly Gln Lys			
865	870	875	880
Pro Asn Leu Leu Asp Arg Leu Arg His Arg Lys Asn Gly Tyr Arg His			
885	890	895	
Leu Lys Asp Ser Asp Glu Glu Asn Val			
900	905		

<210> 3  
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 <212> DNA  
 <213> Human cytomegalovirus

<220>  
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 Met Ala Pro Ser His Val Asp Lys Val Asn Thr Arg Thr Trp Ser Ala  
 1 5 10 15

48

tct atc gtt ttc atg gtg ctg act ttt gtc aac gtc agc gtg cat cta  
 Ser Ile Val Phe Met Val Leu Thr Phe Val Asn Val Ser Val His Leu  
 20 25 30

96

gtg ctg agc aat ttt ccg cac ctg ggc tac ccc tgc gtc tac tat cac

144

Val	Leu	Ser	Asn	Phe	Pro	His	Leu	Gly	Tyr	Pro	Cys	Val	Tyr	Tyr	His	
35					40						45					
gtc	gtg	gac	ttt	gaa	agg	ctc	aac	atg	tcg	gcc	tac	aac	gta	atg	cac	192
Val	Val	Asp	Phe	Glu	Arg	Leu	Asn	Met	Ser	Ala	Tyr	Asn	Val	Met	His	
50						55					60					
ctg	cac	acg	cct	atg	ctt	ttc	tta	gac	tcg	gtg	cag	ttg	gtg	tgc	tac	240
Leu	His	Thr	Pro	Met	Leu	Phe	Leu	Asp	Ser	Val	Gln	Leu	Val	Cys	Tyr	
65						70				75				80		
gcc	gtg	tcc	atg	cag	ctc	gtc	ttt	tta	gcc	gtg	acc	atc	tac	tac	ctg	288
Ala	Val	Phe	Met	Gln	Leu	Val	Phe	Leu	Ala	Val	Thr	Ile	Tyr	Tyr	Leu	
85						90					95					
gta	tgc	tgg	atc	aag	atc	agc	atg	cgc	aag	gac	aaa	ggc	atg	agc	cta	336
Val	Cys	Trp	Ile	Lys	Ile	Ser	Met	Arg	Lys	Asp	Lys	Gly	Met	Ser	Leu	
100						105					110					
aac	cag	tcg	aca	cgc	gac	att	tcg	tac	atg	ggc	gac	agc	ctc	aca	gcc	384
Asn	Gln	Ser	Thr	Arg	Asp	Ile	Ser	Tyr	Met	Gly	Asp	Ser	Leu	Thr	Ala	
115						120					125					
ttc	ctc	tcc	att	ctc	agc	atg	gac	acg	tcc	caa	cta	ttc	aca	ctg	acc	432
Phe	Leu	Phe	Ile	Leu	Ser	Met	Asp	Thr	Phe	Gln	Leu	Phe	Thr	Leu	Thr	
130						135					140					
atg	tca	ttt	cg	ctg	ccc	agc	atg	atc	gcc	tcc	atg	gcc	gcc	gtg	cac	480
Met	Ser	Phe	Arg	Leu	Pro	Ser	Met	Ile	Ala	Phe	Met	Ala	Ala	Val	His	
145						150				155			160			
ttt	ttc	tgc	ctg	acc	att	ttc	aac	gtg	agc	atg	gtc	acg	cag	tac	cgc	528
Phe	Phe	Cys	Leu	Thr	Ile	Phe	Asn	Val	Ser	Met	Val	Thr	Gln	Tyr	Arg	
165						170					175					
agc	tac	aaa	cgc	tca	ctc	ttt	ttc	tcc	tcg	cgt	ctg	cac	ccc	aag	ctc	576
Ser	Tyr	Lys	Arg	Ser	Leu	Phe	Phe	Phe	Ser	Arg	Leu	His	Pro	Lys	Leu	
180						185					190					
aaa	gg	ac	gt	ca	tt	cc	gg	cc	ac	ct	gt	ga	ga	gt	aa	624
Lys	Gly	Thr	Val	Gln	Phe	Arg	Thr	Leu	Ile	Val	Asn	Leu	Val	Glu	Val	
195						200					205					
gcg	ctt	gg	tt	ac	ac	ac	gt	gt	ga	cc	at	gt	cc	tg	tc	672
Ala	Leu	Gly	Phe	Asn	Thr	Thr	Val	Ala	Met	Ala	Leu	Cys	Tyr	Gly		
210						215				220						
ttc	gga	aa	aa	ttt	ttc	gt	ca	gg	cc	ac	at	gt	tt	ga	cc	720
Phe	Gly	Asn	Asn	Phe	Phe	Val	Arg	Thr	Gly	His	Met	Val	Leu	Ala	Val	
225						230				235			240			
ttc	gt	gt	ta	gt	at	at	tcc	at	ta	ttt	tta	ct	at	ga	g	768
Phe	Val	Val	Tyr	Ala	Ile	Ile	Ser	Ile	Ile	Tyr	Phe	Leu	Leu	Ile	Glu	
245						250					255					
gcc	gt	ttt	ttt	ca	ta	gt	aag	gt	ca	tt	cc	tg	ca	ct	gg	816
Ala	Val	Phe	Phe	Gln	Tyr	Val	Lys	Val	Gln	Phe	Gly	Tyr	His	Leu	Gly	

260	265	270	
gcc ttc ttt gga ctc tgc ggc ctc atc tac ccc atc gtg cag tac gat Ala Phe Phe Gly Leu Cys Gly Leu Ile Tyr Pro Ile Val Gln Tyr Asp 275	280	285	864
acc ttc ctc agc aac gaa tac cgc acc ggc atc agc tgg tcg ttc ggc Thr Phe Leu Ser Asn Glu Tyr Arg Thr Gly Ile Ser Trp Ser Phe Gly 290	295	300	912
atg ctc ttt ttc ata tgg gcc atg ttt acg acg tgt cgc gcc gtc cgc Met Leu Phe Phe Ile Trp Ala Met Phe Thr Thr Cys Arg Ala Val Arg 305	310	315	960
tac ttt cgc gga cgc ggt agc ggc agt gtc aag tac cag gcg ctg gcc Tyr Phe Arg Gly Arg Gly Ser Gly Ser Val Lys Tyr Gln Ala Leu Ala 325	330	335	1008
aca gcc tcc ggc gaa gaa gtc gct gtg ctc agt cac cac gac agc ttg Thr Ala Ser Gly Glu Glu Val Ala Val Leu Ser His His Asp Ser Leu 340	345	350	1056
gaa agc cgt cgc ctc cgc gaa gaa gag gac gac gac gat gat gaa gac Glu Ser Arg Arg Leu Arg Glu Glu Asp Asp Asp Asp Glu Asp 355	360	365	1104
ttc gag gac gct taa Phe Glu Asp Ala 370			1119

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Ser Ile Val Phe Met Val Leu Thr Phe Val Asn Val Ser Val His Leu			
20	25	30	
Val Leu Ser Asn Phe Pro His Leu Gly Tyr Pro Cys Val Tyr Tyr His			
35	40	45	
Val Val Asp Phe Glu Arg Leu Asn Met Ser Ala Tyr Asn Val Met His			
50	55	60	
Leu His Thr Pro Met Leu Phe Leu Asp Ser Val Gln Leu Val Cys Tyr			
65	70	75	80
Ala Val Phe Met Gln Leu Val Phe Leu Ala Val Thr Ile Tyr Tyr Leu			
85	90	95	
Val Cys Trp Ile Lys Ile Ser Met Arg Lys Asp Lys Gly Met Ser Leu			
100	105	110	
Asn Gln Ser Thr Arg Asp Ile Ser Tyr Met Gly Asp Ser Leu Thr Ala			
115	120	125	
Phe Leu Phe Ile Leu Ser Met Asp Thr Phe Gln Leu Phe Thr Leu Thr			
130	135	140	
Met Ser Phe Arg Leu Pro Ser Met Ile Ala Phe Met Ala Ala Val His			
145	150	155	160

Phe Phe Cys Leu Thr Ile Phe Asn Val Ser Met Val Thr Gln Tyr Arg  
                          165                         170                         175  
 Ser Tyr Lys Arg Ser Leu Phe Phe Ser Arg Leu His Pro Lys Leu  
                          180                         185                         190  
 Lys Gly Thr Val Gln Phe Arg Thr Leu Ile Val Asn Leu Val Glu Val  
                          195                         200                         205  
 Ala Leu Gly Phe Asn Thr Thr Val Val Ala Met Ala Leu Cys Tyr Gly  
                          210                         215                         220  
 Phe Gly Asn Asn Phe Phe Val Arg Thr Gly His Met Val Leu Ala Val  
                          225                         230                         235                         240  
 Phe Val Val Tyr Ala Ile Ile Ser Ile Ile Tyr Phe Leu Leu Ile Glu  
                          245                         250                         255  
 Ala Val Phe Phe Gln Tyr Val Lys Val Gln Phe Gly Tyr His Leu Gly  
                          260                         265                         270  
 Ala Phe Phe Gly Leu Cys Gly Leu Ile Tyr Pro Ile Val Gln Tyr Asp  
                          275                         280                         285  
 Thr Phe Leu Ser Asn Glu Tyr Arg Thr Gly Ile Ser Trp Ser Phe Gly  
                          290                         295                         300  
 Met Leu Phe Phe Ile Trp Ala Met Phe Thr Thr Cys Arg Ala Val Arg  
                          305                         310                         315                         320  
 Tyr Phe Arg Gly Arg Gly Ser Gly Ser Val Lys Tyr Gln Ala Leu Ala  
                          325                         330                         335  
 Thr Ala Ser Gly Glu Glu Val Ala Val Leu Ser His His Asp Ser Leu  
                          340                         345                         350  
 Glu Ser Arg Arg Leu Arg Glu Glu Asp Asp Asp Asp Asp Glu Asp  
                          355                         360                         365  
 Phe Glu Asp Ala  
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<220>  
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                  1                         5                         10                         15  
  
 gca gag agt tct ggt aac aat tca tcc acg tca acc tct gca act aca                 96  
 Ala Glu Ser Ser Gly Asn Asn Ser Ser Thr Ser Thr Ser Ala Thr Thr  
                  20                         25                         30  
  
 tca aag tct tct gct agc gta tca act acc aaa cta aca aca gtt gca                 144  
 Ser Lys Ser Ser Ala Ser Val Ser Thr Thr Lys Leu Thr Thr Val Ala  
                  35                         40                         45  
  
 aca act tct gca aca act acg acg act acg acc tta tcg aca act agc                 192  
 Thr Thr Ser Ala Thr Thr Thr Thr Thr Thr Leu Ser Thr Thr Ser  
                  50                         55                         60  
  
 act aaa ctc agt tct acc acc cac gat cct aat gtg atg aga cga cat                 240  
 Thr Lys Leu Ser Ser Thr Thr His Asp Pro Asn Val Met Arg Arg His

65	70	75	80	
gcg aac gat gat ttt tac aag gcg cat tgc aca tcg cat atg tat gag				288
Ala Asn Asp Asp Phe Tyr Lys Ala His Cys Thr Ser His Met Tyr Glu				
85	90	95		

ctc tca ctg tcc agc ttt gcg gcc tgg tgg act atg ctt aat gct cta			336
Leu Ser Leu Ser Ser Phe Ala Ala Trp Trp Thr Met Leu Asn Ala Leu			
100	105	110	

att ctc atg gga gct ttt tgt att gta cta cga cat tgc tgc ttc cag			384
Ile Leu Met Gly Ala Phe Cys Ile Val Leu Arg His Cys Cys Phe Gln			
115	120	125	

aac ttt act gca acc acc acc aaa ggc tat tga			417
Asn Phe Thr Ala Thr Thr Lys Gly Tyr			
130	135		

<210> 6

<211> 138

<212> PRT

<213> Human cytomegalovirus

<400> 6

Met Glu Trp Asn Thr Leu Val Leu Gly Leu Leu Val Leu Ser Val Val			
1	5	10	15

Ala Glu Ser Ser Gly Asn Asn Ser Ser Thr Ser Thr Ser Ala Thr Thr			
20	25	30	

Ser Lys Ser Ser Ala Ser Val Ser Thr Thr Lys Leu Thr Thr Val Ala			
35	40	45	

Thr Thr Ser Ala Thr Thr Thr Thr Thr Thr Leu Ser Thr Thr Ser			
50	55	60	

Thr Lys Leu Ser Ser Thr Thr His Asp Pro Asn Val Met Arg Arg His			
65	70	75	80

Ala Asn Asp Asp Phe Tyr Lys Ala His Cys Thr Ser His Met Tyr Glu			
85	90	95	

Leu Ser Leu Ser Ser Phe Ala Ala Trp Trp Thr Met Leu Asn Ala Leu			
100	105	110	

Ile Leu Met Gly Ala Phe Cys Ile Val Leu Arg His Cys Cys Phe Gln			
115	120	125	

Asn Phe Thr Ala Thr Thr Lys Gly Tyr			
130	135		

<210> 7

<211> 2232

<212> DNA

<213> Human cytomegalovirus

<220>

<221> CDS

<222> (1)...(2229)

<400> 7

atg cgg ccc ggc ctc ccc tac ctc act gtc ttc acc gtc tac ctc			48
Met Arg Pro Gly Leu Pro Pro Tyr Leu Thr Val Phe Thr Val Tyr Leu			
1	5	10	15

ctc	agt	cac	cta	cct	tcg	caa	cga	tat	ggc	gcf	gac	gcc	gca	tcc	gaa	96
Leu	Ser	His	Leu	Pro	Ser	Gln	Arg	Tyr	Gly	Ala	Asp	Ala	Ala	Ser	Glu	
20								25					30			
gcf	ctg	gac	cct	cac	gca	ttt	cac	cta	ctc	aac	acc	tac	ggg	aga	144	
Ala	Leu	Asp	Pro	His	Ala	Phe	His	Leu	Leu	Leu	Asn	Thr	Tyr	Gly	Arg	
35								40					45			
ccc	atc	cgc	ttc	ctg	cgt	gaa	aac	acc	cag	tgc	acc	tac	aac	agc	192	
Pro	Ile	Arg	Phe	Leu	Arg	Glu	Asn	Thr	Thr	Gln	Cys	Thr	Tyr	Asn	Ser	
50								55					60			
agc	ctc	cgt	aac	agc	acg	gtc	gtc	agg	gaa	aac	gcc	atc	agt	ttc	aac	240
Ser	Leu	Arg	Asn	Ser	Thr	Val	Val	Arg	Glu	Asn	Ala	Ile	Ser	Phe	Asn	
65								70					75			80
ttt	ttc	caa	agc	tat	aat	caa	tac	tat	gta	ttc	cat	atg	cct	cga	tgt	288
Phe	Phe	Gln	Ser	Tyr	Asn	Gln	Tyr	Tyr	Val	Phe	His	Met	Pro	Arg	Cys	
85								90					95			
ctt	ttt	gcf	ggt	cct	ctg	gcf	gag	cag	ttt	ctg	aac	cag	gta	gat	ctg	336
Leu	Phe	Ala	Gly	Pro	Leu	Ala	Glu	Gln	Phe	Leu	Asn	Gln	Val	Asp	Leu	
100								105					110			
acc	gaa	acc	cta	gaa	aga	tac	caa	cag	aga	ctt	aac	acc	tac	gca	ttg	384
Thr	Glu	Thr	Leu	Glu	Arg	Tyr	Gln	Gln	Arg	Leu	Asn	Thr	Tyr	Ala	Leu	
115								120					125			
gta	tcc	aaa	gac	ctg	gcc	agc	tac	cga	tct	ttt	tcg	cag	cag	ctg	aag	432
Val	Ser	Lys	Asp	Leu	Ala	Ser	Tyr	Arg	Ser	Phe	Ser	Gln	Gln	Leu	Lys	
130								135					140			
gca	caa	gac	agc	ctg	ggt	cag	cag	ccc	acc	acc	gtg	cca	ccg	ccc	att	480
Ala	Gln	Asp	Ser	Leu	Gly	Gln	Gln	Pro	Thr	Thr	Val	Pro	Pro	Pro	Ile	
145								150					155			160
gat	ctg	tca	ata	cct	cac	gtt	tgg	atg	cca	ccc	caa	acc	act	cca	cac	528
Asp	Leu	Ser	Ile	Pro	His	Val	Trp	Met	Pro	Pro	Gln	Thr	Thr	Pro	His	
165								170					175			
gac	tgg	aag	gga	tcg	cac	acc	tcg	gga	cta	cat	cgg	cca	cac	ttt	576	
Asp	Trp	Lys	Gly	Ser	His	Thr	Thr	Ser	Gly	Leu	His	Arg	Pro	His	Phe	
180								185					190			
aac	cag	acc	tgt	atc	ctc	ttt	gat	gga	cac	gat	ctg	ctt	ttc	agc	acc	624
Asn	Gln	Thr	Cys	Ile	Leu	Phe	Asp	Gly	His	Asp	Leu	Leu	Phe	Ser	Thr	
195								200					205			
gtt	acg	ccc	tgt	ctg	cac	cag	ggc	ttt	tac	ctc	atg	gac	gaa	cta	cgt	672
Val	Thr	Pro	Cys	Leu	His	Gln	Gly	Phe	Tyr	Leu	Met	Asp	Glu	Leu	Arg	
210								215					220			
tac	gtt	aaa	atc	aca	ctg	acc	gag	gac	ttc	ttc	gta	gtt	acg	gta	tct	720
Tyr	Val	Lys	Ile	Thr	Leu	Thr	Glu	Asp	Phe	Phe	Val	Val	Thr	Val	Ser	
225								230					235			240

ata gac gac gac aca ccc atg ctg ctt atc ttc ggt cat ctt cca cgc Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg 245 250 255	768
gta ctc ttc aaa gcg ccc tat caa cgc gac aac ttt ata cta cga caa Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln 260 265 270	816
act gaa aaa cac gag ctc ctg gta cta gtt aag aaa gct caa cta aac Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Ala Gln Leu Asn 275 280 285	864
cgt cac tcc tat ctc aaa gac tcg gac ttt ctc gac gcc gca ctc gac Arg His Ser Tyr Leu Lys Asp Ser Asp Phe Leu Asp Ala Ala Leu Asp 290 295 300	912
ttc aac tac ctg gac ctc agc gca ctg tta cgt aac agc ttt cac cgt Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His Arg 305 310 315 320	960
tac gct gta gac gta ctc aaa agc ggt cga tgt caa atg ttg gac cgc Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp Arg 325 330 335	1008
cgc acg gta gaa atg gcc ttc gcc tac gca tta gca ctg ttc gcg gca Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala 340 345 350	1056
gcc cga caa gaa gag gcc ggc acc gaa atc tcc atc cca cga gcc cta Ala Arg Gln Glu Glu Ala Gly Thr Glu Ile Ser Ile Pro Arg Ala Leu 355 360 365	1104
gac cgc cag gcc gca ctc tta caa ata caa gaa ttt atg atc acc tgc Asp Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr Cys 370 375 380	1152
ctc tca caa aca cca cca cgc acc aca ttg ctg cta tat ccc aca gcc Leu Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala 385 390 395 400	1200
gtg gac ctg gcc aaa cga gcc ctc tgg acg ccg gac cag atc acc gac Val Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asp Gln Ile Thr Asp 405 410 415	1248
atc acc agc ctc gta cgc ctg gtc tac ata ctt tct aaa cag aat cag Ile Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln 420 425 430	1296
caa cat ctc att ccc cag tgg gca cta cga cag atc gcc gac ttt gcc Gln His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala 435 440 445	1344
cta caa tta cac aaa acg cac ctg gcc tct ttt ctt tca gcc ttc gcg Leu Gln Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe Ala 450 455 460	1392
cgc caa gaa ctc tac ctc atg ggc agc ctc gtc cac tcc atg ttg gta	1440

Arg Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu Val			
465	470	475	480
cat acg acg gag aga cgc gaa atc ttc atc gta gaa acg ggc ctc tgt			1488
His Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu Cys			
485	490	495	
tca ttg gcc gag cta tca cac ttt acg cag ttg cta gct cat ccg cac			1536
Ser Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro His			
500	505	510	
cac gaa tac ctc agc gac ctg tac aca ccc tgt tcc agt agc ggg cga			1584
His Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg			
515	520	525	
cgc gat cac tcg ctc gaa cgc ctc acg cgt ctc ttc ccc gat gcc acc			1632
Arg Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr			
530	535	540	
gtt cct gct acc gtt ccc gcc ctc tcc atc cta tct acc atg caa			1680
Val Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met Gln			
545	550	555	560
cca agc acg ctg gaa acc ttc ccc gac ctg ttt tgt ctg ccg ctc ggc			1728
Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly			
565	570	575	
gaa tcc ttc tcc gcg cta acc gtc tcc gaa cac gtc agt tat gtc gta			1776
Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Val Val			
580	585	590	
aca aac cag tac ctg atc aaa ggt atc tcc tac cct gtc tcc acc acc			1824
Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr			
595	600	605	
gtc gta ggc cag acg ctc atc atc acc caa acg gac agt caa act aaa			1872
Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr Lys			
610	615	620	
tgc gaa cta acg cgc aac atg cac acc aca cac acg atc aca gcg gcg			1920
Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Ala Ala			
625	630	635	640
ctc aac att tca cta gaa aac tgc gcc ttt tgc caa agc gcc ctg cta			1968
Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu			
645	650	655	
gaa tac gac gac acg caa ggc gtc atc aac atc atg tac atg cac gac			2016
Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His Asp			
660	665	670	
tcg gac gac gtc ctt ttc gcc ctg gat ccc tac aac gaa gtg gtg gtc			2064
Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val Val			
675	680	685	
tca tct ccg cga act cac tac ctc atg ctt ttg aaa aac ggt acg gtc			2112
Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr Val			

690	695	700	
cta gaa gta act gac gtc gtc gtg gac gcc acc gac agt cgt ctc ctc			2160
Leu Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu Leu			
705	710	715	720
atg atg tcc gtc tac gcg cta tcg gcc atc atc ggc atc tat ctg ctc			2208
Met Met Ser Val Tyr Ala Leu Ser Ala Ile Ile Gly Ile Tyr Leu Leu			
725	730	735	
tac cgc atg ctc aag aca tgc tga			2232
Tyr Arg Met Leu Lys Thr Cys			
740			

<210> 8  
 <211> 743  
 <212> PRT  
 <213> Human cytomegalovirus

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 Met Arg Pro Gly Leu Pro Pro Tyr Leu Thr Val Phe Thr Val Tyr Leu  
 1 5 10 15  
 Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser Glu  
 20 25 30  
 Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly Arg  
 35 40 45  
 Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser  
 50 55 60  
 Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn  
 65 70 75 80  
 Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys  
 85 90 95  
 Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu  
 100 105 110  
 Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu  
 115 120 125  
 Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu Lys  
 130 135 140  
 Ala Gln Asp Ser Leu Gly Gln Gln Pro Thr Thr Val Pro Pro Pro Ile  
 145 150 155 160  
 Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His  
 165 170 175  
 Asp Trp Lys Gly Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe  
 180 185 190  
 Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser Thr  
 195 200 205  
 Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Met Asp Glu Leu Arg  
 210 215 220  
 Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val Ser  
 225 230 235 240  
 Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg  
 245 250 255  
 Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln  
 260 265 270  
 Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Ala Gln Leu Asn  
 275 280 285

Arg His Ser Tyr Leu Lys Asp Ser Asp Phe Leu Asp Ala Ala Leu Asp  
 290 295 300  
 Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His Arg  
 305 310 315 320  
 Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp Arg  
 325 330 335  
 Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala  
 340 345 350  
 Ala Arg Gln Glu Ala Gly Thr Glu Ile Ser Ile Pro Arg Ala Leu  
 355 360 365  
 Asp Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr Cys  
 370 375 380  
 Leu Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala  
 385 390 395 400  
 Val Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asp Gln Ile Thr Asp  
 405 410 415  
 Ile Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln  
 420 425 430  
 Gln His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala  
 435 440 445  
 Leu Gln Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe Ala  
 450 455 460  
 Arg Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu Val  
 465 470 475 480  
 His Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu Cys  
 485 490 495  
 Ser Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro His  
 500 505 510  
 His Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg  
 515 520 525  
 Arg Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr  
 530 535 540  
 Val Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met Gln  
 545 550 555 560  
 Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly  
 565 570 575  
 Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Val Val  
 580 585 590  
 Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr  
 595 600 605  
 Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr Lys  
 610 615 620  
 Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Ala Ala  
 625 630 635 640  
 Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu  
 645 650 655  
 Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His Asp  
 660 665 670  
 Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val Val  
 675 680 685  
 Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr Val  
 690 695 700  
 Leu Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu Leu  
 705 710 715 720  
 Met Met Ser Val Tyr Ala Leu Ser Ala Ile Ile Gly Ile Tyr Leu Leu  
 725 730 735  
 Tyr Arg Met Leu Lys Thr Cys

740

<210> 9  
 <211> 921  
 <212> DNA  
 <213> Human cytomegalovirus

<220>  
 <221> CDS  
 <222> (1)...(918)

<400> 9

cgt ttt agg gat cga aga cct gag	cgc caa ctt tcg	gcf cca act ggc	48
Arg Phe Arg Asp Arg Arg	Pro Glu Arg Gln	Leu Ser Ala Pro	Thr Gly
1	5	10	15

tcc tta ccg tca cac tct cat	cgt gcc gca gac	ttg atg tgc	cgc cgc	96
Ser Leu Pro Ser His Ser His	Arg Ala Ala Asp	Leu Met Cys	Arg Arg	
20	25	30		

ccg gat tgc ggc ttc tct	ttc tca cct gga	ccg gtg gta	ctg ctg tgg	144
Pro Asp Cys Gly Phe Ser	Phe Ser Pro Gly	Pro Val Val	Leu Leu Trp	
35	40	45		

tgt tgc ctt ctg ctg ccc	att gtt tcc tca gtc	gcc gtc agc	gtc gct	192
Cys Cys Leu Leu Pro Ile	Val Ser Ser Val	Ala Val Ser	Val Ala	
50	55	60		

cct acc gcc gcc gag	aaa gtc ccc	gag tgc	ccc gaa cta acg	cgt	240
Pro Thr Ala Ala Glu Lys	Val Pro Ala Glu Cys	Pro Glu Leu	Thr Arg		
65	70	75	80		

cga tgc ctg ttg ggt	gag gtg ttt	cag ggt	gac aag tat	gaa agt tgg	288
Arg Cys Leu Leu Gly	Glu Val Phe	Gln Gly	Asp Lys Tyr	Glu Ser Trp	
85	90		95		

ctg cgc ccg ttg gtg	aat gtt acc aga	cgc gat	gcc ccg	cta tcg caa	336
Leu Arg Pro Leu Val Asn	Val Thr Arg Arg	Asp Gly	Pro Leu Ser	Gln	
100	105		110		

ctt att cgt tac cgt	ccc gtt acg	ccg gag	gcc aac	tcc gtg ctg	384
Leu Ile Arg Tyr Arg	Pro Val Thr Pro	Glu Ala	Asn Ser	Val Leu	
115	120		125		

ttg gac gat gct ttc	ctg gac act	ctg gcc	ctg tac	aac aat	ccg	432
Leu Asp Asp Ala Phe	Leu Asp Thr	Leu Ala	Leu Leu	Tyr Asn Asn	Pro	
130	135		140			

gat caa ttg cgg gcc	ctg ctg acg	ctg ttg	agc tcg	gac aca	gcf ccg	480
Asp Gln Leu Arg Ala	Leu Thr Leu Leu	Ser Ser Asp	Thr Ala	Pro		
145	150		155	160		

cgc tgg atg acg	gtg atg cgc	ggc tac	agc gag	tgc ggc	gat ggc	528
Arg Trp Met Thr Val	Met Arg Gly	Tyr Ser	Glu Cys	Gly Asp	Gly Ser	
165	170		175			

ccg gcc gtg tac acg	tgc gtg gac	gac ctg	tgc cgc	ggc tac	gac ctc	576
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Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys Arg Gly Tyr Asp Leu			
180	185	190	
acg cga ctg tca tac ggg cgc agc atc ttc acg gaa cac gtg tta ggc		624	
Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr Glu His Val Leu Gly			
195	200	205	
ttc gag ctg gtg cca ccg tct ctc ttt aac gtg gtg gtg gcc ata cgc		672	
Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val Val Val Ala Ile Arg			
210	215	220	
aac gaa gcc acg cgt acc aac cgc gcc gtg cgt ctg ccc gtg agc acc		720	
Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg Leu Pro Val Ser Thr			
225	230	235	240
gct gcc gcg ccc gag ggc atc aca ctc ttt tac ggc ctg tac aac gca		768	
Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe Tyr Gly Leu Tyr Asn Ala			
245	250	255	
gtg aag gaa ttc tgc ctg cgt cac cag ctg gac ccg ccg cta cta cgc		816	
Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp Pro Pro Leu Leu Arg			
260	265	270	
cac cta gat aaa tac tac gcc gga ctg ccg ccc gag ctg aag cag acg		864	
His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro Glu Leu Lys Gln Thr			
275	280	285	
cgc gtc aac ctg ccg gct cac tcg cgc tat ggc cct caa gca gtg gat		912	
Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly Pro Gln Ala Val Asp			
290	295	300	
gct cgc taa		921	
Ala Arg			
305			

<210> 10  
 <211> 306  
 <212> PRT  
 <213> Human cytomegalovirus

<400> 10  
 Arg Phe Arg Asp Arg Arg Pro Glu Arg Gln Leu Ser Ala Pro Thr Gly  
 1 5 10 15  
 Ser Leu Pro Ser His Ser His Arg Ala Ala Asp Leu Met Cys Arg Arg  
 20 25 30  
 Pro Asp Cys Gly Phe Ser Phe Ser Pro Gly Pro Val Val Leu Leu Trp  
 35 40 45  
 Cys Cys Leu Leu Leu Pro Ile Val Ser Ser Val Ala Val Ser Val Ala  
 50 55 60  
 Pro Thr Ala Ala Glu Lys Val Pro Ala Glu Cys Pro Glu Leu Thr Arg  
 65 70 75 80  
 Arg Cys Leu Leu Gly Glu Val Phe Gln Gly Asp Lys Tyr Glu Ser Trp  
 85 90 95  
 Leu Arg Pro Leu Val Asn Val Thr Arg Arg Asp Gly Pro Leu Ser Gln  
 100 105 110  
 Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala Ala Asn Ser Val Leu

115	120	125	
Leu Asp Asp Ala Phe Leu Asp Thr Leu Ala Leu	Leu Tyr Asn Asn Pro		
130	135	140	
Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser	Ser Ser Asp Thr Ala Pro		
145	150	155	160
Arg Trp Met Thr Val Met Arg Gly Tyr Ser	Glu Cys Gly Asp Gly Ser		
165	170	175	
Pro Ala Val Tyr Thr Cys Val Asp Asp	Leu Cys Arg Gly Tyr Asp Leu		
180	185	190	
Thr Arg Leu Ser Tyr Gly Arg Ser	Ile Phe Thr Glu His Val Leu Gly		
195	200	205	
Phe Glu Leu Val Pro Pro Ser	Leu Phe Asn Val Val Val Ala Ile Arg		
210	215	220	
Asn Glu Ala Thr Arg Thr Asn Arg Ala Val	Arg Leu Pro Val Ser Thr		
225	230	235	240
Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe	Tyr Gly Leu Tyr Asn Ala		
245	250	255	
Val Lys Glu Phe Cys Leu Arg His Gln	Leu Asp Pro Pro Leu Leu Arg		
260	265	270	
His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro	Pro Glu Leu Lys Gln Thr		
275	280	285	
Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly	Pro Gln Ala Val Asp		
290	295	300	
Ala Arg			
305			

<210> 11  
 <211> 1401  
 <212> DNA  
 <213> Human cytomegalovirus

<220>  
 <221> CDS  
 <222> (1)...(1398)

<400> 11			
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Met Gly Arg Lys Glu Met Met Val Arg Asp Val Pro Lys Met Val Phe			
1	5	10	15
ct a ta tct ata tct ttc ttg ctt gtt tct ttc ata aac tgt aaa gtt			96
Leu Ile Ser Ile Ser Phe Leu Leu Val Ser Phe Ile Asn Cys Lys Val			
20	25	30	
atg tca aaa gcg ctt tat aat cgt cct tgg agg ggc ttg gta ctg tct			144
Met Ser Lys Ala Leu Tyr Asn Arg Pro Trp Arg Gly Leu Val Leu Ser			
35	40	45	
aag ata ggc aaa tat aaa tta gat cag ctt aag tta gaa att ttg aga			192
Lys Ile Gly Lys Tyr Lys Leu Asp Gln Leu Lys Leu Glu Ile Leu Arg			
50	55	60	
caa cta gaa acg act att tct aca aaa tac aat gta agt aaa caa ccg			240
Gln Leu Glu Thr Thr Ile Ser Thr Lys Tyr Asn Val Ser Lys Gln Pro			
65	70	75	80
gtt aaa aat ctc act atg aac atg aca gag ttt cca caa tac tac att			288

Val Lys Asn Leu Thr Met Asn Met Thr Glu Phe Pro Gln Tyr Tyr Ile			
85	90	95	
tta gcg ggc ccc att cag aat tat agt ata acc tat ctg tgg ttt gat			336
Leu Ala Gly Pro Ile Gln Asn Tyr Ser Ile Thr Tyr Leu Trp Phe Asp			
100	105	110	
ttt tat agt acc cag ctt aga aaa ccc gca aaa tac gtt tac tca cag			384
Phe Tyr Ser Thr Gln Leu Arg Lys Pro Ala Lys Tyr Val Tyr Ser Gln			
115	120	125	
tac aat cat acg gct aaa acg ata aca ttc aga ccc cca cct tgt ggt			432
Tyr Asn His Thr Ala Lys Thr Ile Thr Phe Arg Pro Pro Pro Cys Gly			
130	135	140	
act gtg cct tcc atg act tgt ctt tcc gaa atg cta aac gtt tcc aaa			480
Thr Val Pro Ser Met Thr Cys Leu Ser Glu Met Leu Asn Val Ser Lys			
145	150	155	160
cgt aat gat act ggc gaa caa ggt tgc ggt aat ttc acc acg ttc aac			528
Arg Asn Asp Thr Gly Glu Gln Gly Cys Gly Asn Phe Thr Thr Phe Asn			
165	170	175	
ccc atg ttt ttc aat gta ccg cgt tgg aac acc aaa ttg tac gtg ggt			576
Pro Met Phe Asn Val Pro Arg Trp Asn Thr Lys Leu Tyr Val Gly			
180	185	190	
ccg act aag gtt aac gta gat agt caa acg att tat ttt cta ggt tta			624
Pro Thr Lys Val Asn Val Asp Ser Gln Thr Ile Tyr Phe Leu Gly Leu			
195	200	205	
acc gcc ctg ctt tta cgt tac gca caa cgc aac tgt aca cac agt ttc			672
Thr Ala Leu Leu Arg Tyr Ala Gln Arg Asn Cys Thr His Ser Phe			
210	215	220	
tac ctg gtt aac gcc atg agc cgg aat cta ttt cgc gtc ccc aag tat			720
Tyr Leu Val Asn Ala Met Ser Arg Asn Leu Phe Arg Val Pro Lys Tyr			
225	230	235	240
att aac ggc acc aag tta aaa aac act atg cga aaa cta aaa cgt aaa			768
Ile Asn Gly Thr Lys Leu Lys Asn Thr Met Arg Lys Leu Lys Arg Lys			
245	250	255	
caa gcg ccc gtt aag gaa caa ttc gaa aaa aaa gct aag aaa act cag			816
Gln Ala Pro Val Lys Glu Gln Phe Glu Lys Lys Ala Lys Lys Thr Gln			
260	265	270	
agt act act acg cca tac ttt tcc tat aca acg tct gcc gct ctc aac			864
Ser Thr Thr Pro Tyr Phe Ser Tyr Thr Ser Ala Ala Leu Asn			
275	280	285	
gtc act act aac gtg act tat agt att act acc gcc gca agg cgg gtt			912
Val Thr Thr Asn Val Thr Tyr Ser Ile Thr Thr Ala Ala Arg Arg Val			
290	295	300	
tcc acg tct aca att gct tat cgt cct gat agc agc ttt atg aag tcc			960
Ser Thr Ser Thr Ile Ala Tyr Arg Pro Asp Ser Ser Phe Met Lys Ser			

305	310	315	320	
att atg gcc aca cag tta agg gac cta gca acg tgg gtg tat acc act Ile Met Ala Thr Gln Leu Arg Asp Leu Ala Thr Trp Val Tyr Thr Thr 325		330		335
1008				
cta cgt tac cgg caa aat cct ttt tgt gaa cca agc cgc aac cga acc Leu Arg Tyr Arg Gln Asn Pro Phe Cys Glu Pro Ser Arg Asn Arg Thr 340		345		350
1056				
gcc gtg tca gaa ttt atg aaa aac acg cac gta cta atc cgt aac gaa Ala Val Ser Glu Phe Met Lys Asn Thr His Val Leu Ile Arg Asn Glu 355		360		365
1104				
acg ccg tac act att tac ggt act ctc gac atg agc tcc tta tat tac Thr Pro Tyr Thr Ile Tyr Gly Thr Leu Asp Met Ser Ser Leu Tyr Tyr 370		375		380
1152				
aac gaa acc atg ttc gtg gaa aac aaa aca gct tcc gat agt aac aaa Asn Glu Thr Met Phe Val Glu Asn Lys Thr Ala Ser Asp Ser Asn Lys 385		390		395
1200				
act aca cct acg tca cca tca atg ggg ttt cag aga aca ttt ata gat Thr Thr Pro Thr Ser Pro Ser Met Gly Phe Gln Arg Thr Phe Ile Asp 405		410		415
1248				
ccc ctg tgg gac tat cta gac tcg ctg ttt cta gat gag att cgt Pro Leu Trp Asp Tyr Leu Asp Ser Leu Leu Phe Leu Asp Glu Ile Arg 420		425		430
1296				
aac ttt agc ctc cgg tca ccc acg tat gta aac ctt acc ccg ccg gaa Asn Phe Ser Leu Arg Ser Pro Thr Tyr Val Asn Leu Thr Pro Pro Glu 435		440		445
1344				
cac ccg cgg gct gta aat ctg tcc acc ctc aat agc ctt tgg tgg tgg His Arg Arg Ala Val Asn Leu Ser Thr Leu Asn Ser Leu Trp Trp Trp 450		455		460
1392				
ttg cag taa Leu Gln 465				1401

<210> 12  
 <211> 466  
 <212> PRT  
 <213> Human cytomegalovirus

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 20 25 30  
 Met Ser Lys Ala Leu Tyr Asn Arg Pro Trp Arg Gly Leu Val Leu Ser  
 35 40 45  
 Lys Ile Gly Lys Tyr Lys Leu Asp Gln Leu Lys Leu Glu Ile Leu Arg  
 50 55 60

Gln Leu Glu Thr Thr Ile Ser Thr Lys Tyr Asn Val Ser Lys Gln Pro  
 65 70 75 80  
 Val Lys Asn Leu Thr Met Asn Met Thr Glu Phe Pro Gln Tyr Tyr Ile  
 85 90 95  
 Leu Ala Gly Pro Ile Gln Asn Tyr Ser Ile Thr Tyr Leu Trp Phe Asp  
 100 105 110  
 Phe Tyr Ser Thr Gln Leu Arg Lys Pro Ala Lys Tyr Val Tyr Ser Gln  
 115 120 125  
 Tyr Asn His Thr Ala Lys Thr Ile Thr Phe Arg Pro Pro Pro Cys Gly  
 130 135 140  
 Thr Val Pro Ser Met Thr Cys Leu Ser Glu Met Leu Asn Val Ser Lys  
 145 150 155 160  
 Arg Asn Asp Thr Gly Glu Gln Gly Cys Gly Asn Phe Thr Thr Phe Asn  
 165 170 175  
 Pro Met Phe Phe Asn Val Pro Arg Trp Asn Thr Lys Leu Tyr Val Gly  
 180 185 190  
 Pro Thr Lys Val Asn Val Asp Ser Gln Thr Ile Tyr Phe Leu Gly Leu  
 195 200 205  
 Thr Ala Leu Leu Leu Arg Tyr Ala Gln Arg Asn Cys Thr His Ser Phe  
 210 215 220  
 Tyr Leu Val Asn Ala Met Ser Arg Asn Leu Phe Arg Val Pro Lys Tyr  
 225 230 235 240  
 Ile Asn Gly Thr Lys Leu Lys Asn Thr Met Arg Lys Leu Lys Arg Lys  
 245 250 255  
 Gln Ala Pro Val Lys Glu Gln Phe Glu Lys Lys Ala Lys Lys Thr Gln  
 260 265 270  
 Ser Thr Thr Pro Tyr Phe Ser Tyr Thr Ser Ala Ala Leu Asn  
 275 280 285  
 Val Thr Thr Asn Val Thr Tyr Ser Ile Thr Thr Ala Ala Arg Arg Val  
 290 295 300  
 Ser Thr Ser Thr Ile Ala Tyr Arg Pro Asp Ser Ser Phe Met Lys Ser  
 305 310 315 320  
 Ile Met Ala Thr Gln Leu Arg Asp Leu Ala Thr Trp Val Tyr Thr Thr  
 325 330 335  
 Leu Arg Tyr Arg Gln Asn Pro Phe Cys Glu Pro Ser Arg Asn Arg Thr  
 340 345 350  
 Ala Val Ser Glu Phe Met Lys Asn Thr His Val Leu Ile Arg Asn Glu  
 355 360 365  
 Thr Pro Tyr Thr Ile Tyr Gly Thr Leu Asp Met Ser Ser Leu Tyr Tyr  
 370 375 380  
 Asn Glu Thr Met Phe Val Glu Asn Lys Thr Ala Ser Asp Ser Asn Lys  
 385 390 395 400  
 Thr Thr Pro Thr Ser Pro Ser Met Gly Phe Gln Arg Thr Phe Ile Asp  
 405 410 415  
 Pro Leu Trp Asp Tyr Leu Asp Ser Leu Leu Phe Leu Asp Glu Ile Arg  
 420 425 430  
 Asn Phe Ser Leu Arg Ser Pro Thr Tyr Val Asn Leu Thr Pro Pro Glu  
 435 440 445  
 His Arg Arg Ala Val Asn Leu Ser Thr Leu Asn Ser Leu Trp Trp Trp  
 450 455 460  
 Leu Gln  
 465

<210> 13  
 <211> 1686  
 <212> DNA  
 <213> Human cytomegalovirus

<220>  
 <221> CDS  
 <222> (1)...(1683)

<400> 13

atg	gag	tcg	cgc	ggt	cgc	cgt	tgt	ccc	gaa	atg	ata	tcc	gta	ctg	ggt	48
Met	Glu	Ser	Arg	Gly	Arg	Arg	Cys	Pro	Glu	Met	Ile	Ser	Val	Leu	Gly	
1		5						10						15		

ccc att tcg ggg cac gtg ctg aaa gcc gtg ttt agt cgc ggc gat acg

Pro	Ile	Ser	Gly	His	Val	Leu	Lys	Ala	Val	Phe	Ser	Arg	Gly	Asp	Thr	96
20					25							30				

ccg gtg ctg ccg cac gag acg cga ctc ctg cag acg ggt atc cac gta

Pro	Val	Leu	Pro	His	Glu	Thr	Arg	Leu	Leu	Gln	Thr	Gly	Ile	His	Val	144
35					40						45					

cgc gtg agc cag ccc tcg ctg atc ttg gta tcg cag tac acg ccc gac

Arg	Val	Ser	Gln	Pro	Ser	Leu	Ile	Leu	Val	Ser	Gln	Tyr	Thr	Pro	Asp	192
50					55					60						

tcg acg cca tgc cac cgc ggc gac aat cag ctg cag gtg cag cac acg

Ser	Thr	Pro	Cys	His	Arg	Gly	Asp	Asn	Gln	Leu	Gln	Val	Gln	His	Thr	240
65					70					75			80			

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 tac ttt acg ggc agc gag gtg gag aac gtg tcg gtc aac gtg cac aac

Tyr	Phe	Thr	Gly	Ser	Glu	Val	Glu	Asn	Val	Ser	Val	Asn	Val	His	Asn	288
85					90					95						

ccc acg ggc cga agc atc tgc ccc agc cag gag ccc atg tcg atc tat

Pro	Thr	Gly	Arg	Ser	Ile	Cys	Pro	Ser	Gln	Glu	Pro	Met	Ser	Ile	Tyr	336
100						105					110					

gtg tac gcg ctg ccg ctc aag atg ctg aac atc ccc agc atc aac gtg

Val	Tyr	Ala	Leu	Pro	Leu	Lys	Met	Leu	Asn	Ile	Pro	Ser	Ile	Asn	Val	384
115					120					125						

cac cac tac ccg tcg gcg gcc gag cgc aaa cac cga cac ctg ccc gta

His	His	Tyr	Pro	Ser	Ala	Ala	Glu	Arg	Lys	His	Arg	His	Leu	Pro	Val	432
130					135					140						

gct gac gct gtg att cac gcg tcg ggc aag cag atg tgg cag gcg cgt

Ala	Asp	Ala	Val	Ile	His	Ala	Ser	Gly	Lys	Gln	Met	Trp	Gln	Ala	Arg	480
145					150					155			160			

ctc acg gtc tcg gga ctg gcc tgg acg cgt cag cag aac cag tgg aaa

Leu	Thr	Val	Ser	Gly	Leu	Ala	Trp	Thr	Arg	Gln	Gln	Asn	Gln	Trp	Lys	528
165						170					175					

gag ccc gac gtc tac tac acg tca gcg ttc gtg ttt ccc acc aag gac

Glu	Pro	Asp	Val	Tyr	Tyr	Ser	Ala	Phe	Val	Phe	Pro	Thr	Lys	Asp	576
180						185					190				

gtg gca ctg cgg cac gtg gtg tgc gcg cac gag ctg gtt tgc tcc atg

Val	Ala	Leu	Arg	His	Val	Val	Cys	Ala	His	Glu	Leu	Val	Cys	Ser	Met	624
195					200					205						

gag aac acg cgc gca acc aag atg cag gtg ata ggt gac cag tac gtc		672
Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val		
210	215	220
aag gtg tac ctg gag tcc ttc tgc gag gac gtg ccc tcc ggc aag ctc		720
Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu		
225	230	235
240		
ttt atg cac gtc acg ctg ggc tct gac gtg gaa gag gac ctg acg atg		768
Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met		
245	250	255
acc cgc aac ccg caa ccc ttc atg cgc ccc cac gag cgc aac ggc ttt		816
Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe		
260	265	270
acg gtg ttg tgt ccc aaa aat atg ata atc aaa ccg ggc aag atc tcg		864
Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser		
275	280	285
cac atc atg ctg gat gtg gct ttt acc tca cac gag cat ttt ggg ctg		912
His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu		
290	295	300
ctg tgt ccc aag agc atc ccg ggc ctg agc atc tca ggt aac ctg ttg		960
Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu		
305	310	315
320		
atg aac ggg cag cag atc ttc ctg gag gta caa gcc ata cgc gag acc		1008
Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr		
325	330	335
gtg gaa ctg cgt cag tac gat ccc gtg gct gcg ctc ttc ttt ttc gat		1056
Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Asp		
340	345	350
atc gac ttg ctg ctg cag cgc ggg cct cag tac agc gag cac ccc acc		1104
Ile Asp Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr		
355	360	365
ttc acc agc cag tat cgc atc cag ggc aag ctt gag tac cga cac acc		1152
Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr		
370	375	380
380		
tgg gac cgg cac gac gag ggt gcc gcc cag ggc gac gac gtc tgg		1200
Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp		
385	390	395
400		
acc agc gga tcg gac tcc gac gaa gaa ctc gta acc acc gag cgc aag		1248
Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys		
405	410	415
415		
acg ccc cgc gtc acc ggc ggc gcc atg gcg ggc gcc tcc act tcc		1296
Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala Ser Thr Ser		
420	425	430

gcf ggc cgc aaa cgc aaa tca gca tcc tcg gcf acg gcf tgc acg tcg	1344
Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser	
435 440 445	
gcf gtt atg aca cgc ggc cgc ctt aag gcc gag tcc acc gtc gcf ccc	1392
Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro	
450 455 460	
gaa gag gac acc gac gag gat tcc gac aac gaa atc cac aat ccg gcc	1440
Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala	
465 470 475 480	
gtg ttc acc tgg ccc tgg cag gcc ggc atc ctg gcc cgc aac ctg	1488
Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu	
485 490 495	
gtg ccc atg gtg gct acg gtt cag ggt cag aat ctg aag tac cag gaa	1536
Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu	
500 505 510	
ttc ttc tgg gac gcc aac gac atc tac cgc atc ttc gcc gaa ttg gaa	1584
Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu	
515 520 525	
ggc gta tgg cag ccc gct gcf caa ccc aaa cgt cgc cgc cac cgg caa	1632
Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln	
530 535 540	
gac gcc ttg ccc ggg cca tgc atc gcc tcg acg ccc aaa aag cac cga	1680
Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg	
545 550 555 560	
ggt tga	1686
Gly	

<210> 14  
 <211> 561  
 <212> PRT  
 <213> Human cytomegalovirus

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 1 5 10 15  
 Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr  
 20 25 30  
 Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val  
 35 40 45  
 Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp  
 50 55 60  
 Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr  
 65 70 75 80  
 Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn  
 85 90 95  
 Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr  
 100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val  
 115 120 125  
 His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val  
 130 135 140  
 Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg  
 145 150 155 160  
 Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys  
 165 170 175  
 Glu Pro Asp Val Tyr Tyr Ser Ala Phe Val Phe Pro Thr Lys Asp  
 180 185 190  
 Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met  
 195 200 205  
 Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val  
 210 215 220  
 Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu  
 225 230 235 240  
 Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met  
 245 250 255  
 Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe  
 260 265 270  
 Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser  
 275 280 285  
 His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu  
 290 295 300  
 Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu  
 305 310 315 320  
 Met Asn Gly Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr  
 325 330 335  
 Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Asp  
 340 345 350  
 Ile Asp Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr  
 355 360 365  
 Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr  
 370 375 380  
 Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp  
 385 390 395 400  
 Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys  
 405 410 415  
 Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala Ser Thr Ser  
 420 425 430  
 Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser  
 435 440 445  
 Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro  
 450 455 460  
 Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala  
 465 470 475 480  
 Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu  
 485 490 495  
 Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu  
 500 505 510  
 Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu  
 515 520 525  
 Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln  
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 545 550 555 560  
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<210> 15  
<211> 3147  
<212> DNA  
<213> Human cytomegalovirus

<220>  
<221> CDS  
<222> (1)...(3144)

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 1 5 10 15  
  
 gtc aac ttt ctg cgc cat ctc acg caa aag ccc gac gtc gat ctc gag 96  
 Val Asn Phe Leu Arg His Leu Thr Gln Lys Pro Asp Val Asp Leu Glu  
 20 25 30  
  
 gca cac ccc aag atc ctg aaa aaa tgt ggc gaa aaa cgc ctg cac cgg 144  
 Ala His Pro Lys Ile Leu Lys Lys Cys Gly Glu Lys Arg Leu His Arg  
 35 40 45  
  
 cgt acg gtg ctg ttc aac gag ctc atg ctt tgg ttg gga tac tac cgc 192  
 Arg Thr Val Leu Phe Asn Glu Leu Met Leu Trp Leu Gly Tyr Tyr Arg  
 50 55 60  
  
 gag ctg cgt ttt cac aac ccc gac ctc tcc tca gtg ctc gag gag ttc 240  
 Glu Leu Arg Phe His Asn Pro Asp Leu Ser Ser Val Leu Glu Glu Phe  
 65 70 75 80  
  
 gag gtg cgt tgc gtg gcc gtg gcg cgt cgc ggc tac act tac ccg ttc 288  
 Glu Val Arg Cys Val Ala Val Ala Arg Arg Gly Tyr Thr Tyr Pro Phe  
 85 90 95  
  
 ggt gat cgt ggt aag gcg cgt gac cac ctg gct gtg cta gac cgt acc 336  
 Gly Asp Arg Gly Lys Ala Arg Asp His Leu Ala Val Leu Asp Arg Thr  
 100 105 110  
  
 gaa ttc gat acg gac gtg cgc cac gat gcc gag atc gtg gaa cgc gcg 384  
 Glu Phe Asp Thr Asp Val Arg His Asp Ala Glu Ile Val Glu Arg Ala  
 115 120 125  
  
 ctc gta agc gcg gtc att ctg gcc aag atg tcg gtg cgc gag acg ctg 432  
 Leu Val Ser Ala Val Ile Leu Ala Lys Met Ser Val Arg Glu Thr Leu  
 130 135 140  
  
 gtc aca gcc atc ggc cag acg gaa ccc atc gcc ttt gtg cac ctc aag 480  
 Val Thr Ala Ile Gly Gln Thr Glu Pro Ile Ala Phe Val His Leu Lys  
 145 150 155 160  
  
 gat acg gag gtg cag cgc att gaa gaa aac ctg gag ggt gtg cgc cgt 528  
 Asp Thr Glu Val Gln Arg Ile Glu Glu Asn Leu Glu Gly Val Arg Arg  
 165 170 175  
  
 aac atg ttc tgc gtg aaa ccg ctc gac ctt aac ctg gac cgg cac gcc 576

Asn Met Phe Cys Val Lys Pro Leu Asp Leu Asn Leu Asp Arg His Ala			
180	185	190	
aac acg gcg ctg gtc aac gcc gtc aac aag ctc gtg tac acg ggc cgt			624
Asn Thr Ala Leu Val Asn Ala Val Asn Lys Leu Val Tyr Thr Gly Arg			
195	200	205	
ctc atc atg aac gtg cgc agg tct tgg gag gag ctg gag cgc aaa tgt			672
Leu Ile Met Asn Val Arg Arg Ser Trp Glu Glu Leu Glu Arg Lys Cys			
210	215	220	
ctg gcg cgc att cag gag cgc tgc aag ctg ctg gtc aag gag ctg cgc			720
Leu Ala Arg Ile Gln Glu Arg Cys Lys Leu Leu Val Lys Glu Leu Arg			
225	230	235	240
atg tgc ctt tcc ttt gat tcc aac tac tgt cgc aat atc ctc aag cac			768
Met Cys Leu Ser Phe Asp Ser Asn Tyr Cys Arg Asn Ile Leu Lys His			
245	250	255	
gcc gtg gaa aac ggc gac tcg gcc gac acg ctg ttg gag ctg ctc atc			816
Ala Val Glu Asn Gly Asp Ser Ala Asp Thr Leu Leu Glu Leu Leu Ile			
260	265	270	
gag gac ttt gat atc tac gtg gac agc ttc cca cag tcg gcg cac acg			864
Glu Asp Phe Asp Ile Tyr Val Asp Ser Phe Pro Gln Ser Ala His Thr			
275	280	285	
ttt ttg ggc gcg cgc tcg ccg tcg ttg gag ttt gac gat gac gcc aat			912
Phe Leu Gly Ala Arg Ser Pro Ser Leu Glu Phe Asp Asp Asp Ala Asn			
290	295	300	
ctc ctc tcg ctc ggc ggc ggt tcg gcc ttc tcg tcg gta ccc aag aaa			960
Leu Leu Ser Leu Gly Gly Ser Ala Phe Ser Ser Val Pro Lys Lys			
305	310	315	320
cat gtc ccc acg cag ccg ctg gac ggc tgg agc tgg atc gcc agt ccc			1008
His Val Pro Thr Gln Pro Leu Asp Gly Trp Ser Trp Ile Ala Ser Pro			
325	330	335	
tgg aag gga cac aaa ccg ttc cgc ttc gag gcc cat ggt tct ctg gca			1056
Trp Lys Gly His Lys Pro Phe Arg Phe Glu Ala His Gly Ser Leu Ala			
340	345	350	
ccg gcc gaa gcc cac gct gcc cgt tcg gcg gcc gtc ggc tat tac			1104
Pro Ala Ala Glu Ala His Ala Ala Arg Ser Ala Ala Val Gly Tyr Tyr			
355	360	365	
gac gaa gag gaa aag cgt cgc gag cgg cag aaa cgg gtg gac gac gag			1152
Asp Glu Glu Glu Lys Arg Arg Glu Arg Gln Lys Arg Val Asp Asp Glu			
370	375	380	
gtg gtg cag cgt gag aaa cag cag ctg aag gct tgg gag gag agg cag			1200
Val Val Gln Arg Glu Lys Gln Gln Leu Lys Ala Trp Glu Glu Arg Gln			
385	390	395	400
cag aac ctg cag caa cgt cag cag caa cca ccg ccc ccg gca cgt aaa			1248
Gln Asn Leu Gln Gln Arg Gln Gln Pro Pro Pro Ala Arg Lys			

405	410	415	
ccg agc gcc tcc cg <sup>g</sup> agg ctc ttt ggc tcc agt gcc gat gag gac gac Pro Ser Ala Ser Arg Arg Leu Phe Gly Ser Ser Ala Asp Glu Asp Asp			1296
420	425	430	
gac gat gat gat gac gag aaa aac atc ttt acg ccc atc aag aaa ccg Asp Asp Asp Asp Asp Glu Lys Asn Ile Phe Thr Pro Ile Lys Lys Pro			1344
435	440	445	
gga act agc ggc aag ggc gcc gct agt ggt ggc ggt gtt tcc agc att Gly Thr Ser Gly Lys Gly Ala Ala Ser Gly Gly Val Ser Ser Ile			1392
450	455	460	
ttc agc ggc ctg tta tcc tcg ggc agt cag aaa ccg acc agc ggt ccc Phe Ser Gly Leu Leu Ser Ser Gly Ser Gln Lys Pro Thr Ser Gly Pro			1440
465	470	475	480
ttg aac atc ccg caa caa caa cag cgt cac gcg gct ttc agt ctc gtc Leu Asn Ile Pro Gln Gln Gln Arg His Ala Ala Phe Ser Leu Val			1488
485	490	495	
tcc ccg cag gtg acc aag gcc agc ccg gga agg gtc cgt cgg gac agc Ser Pro Gln Val Thr Lys Ala Ser Pro Gly Arg Val Arg Arg Asp Ser			1536
500	505	510	
gcg tgg gac gtg agg ccg ctc acg gag acc aga ggg gat ctt ttc tcg Ala Trp Asp Val Arg Pro Leu Thr Glu Thr Arg Gly Asp Leu Phe Ser			1584
515	520	525	
ggc gac gag gat tcc gac agc tcg gat ggc tat ccc ccc aac cgt caa Gly Asp Glu Asp Ser Asp Ser Ser Asp Gly Tyr Pro Pro Asn Arg Gln			1632
530	535	540	
gat ccg cgt ttc acc gac acg ctg gtg gac atc acg gat acc gag acg Asp Pro Arg Phe Thr Asp Thr Leu Val Asp Ile Thr Asp Thr Glu Thr			1680
545	550	555	560
agc gcc aaa ccg ccc gtc acc acc gcg tac aag ttc gag caa ccg acg Ser Ala Lys Pro Pro Val Thr Thr Ala Tyr Lys Phe Glu Gln Pro Thr			1728
565	570	575	
ttg acg ttc ggc gcc gga gtt aac gtt cct gct ggc gcc ggc gct gcc Leu Thr Phe Gly Ala Gly Val Asn Val Pro Ala Gly Ala Gly Ala Ala			1776
580	585	590	
atc ctc acg ccg acg cct gtc aat cct tcc acg gcc ccc gct ccg gcc Ile Leu Thr Pro Thr Pro Val Asn Pro Ser Thr Ala Pro Ala Pro Ala			1824
595	600	605	
ccg aca cct acc ttc gcg ggt acc caa acc ccg gtc aac ggt aac tcg Pro Thr Pro Thr Phe Ala Gly Thr Gln Thr Pro Val Asn Gly Asn Ser			1872
610	615	620	
ccc tgg gct ccg acg gcg ccg ttg ccc ggg gat atg aac ccc gcc aac Pro Trp Ala Pro Thr Ala Pro Leu Pro Gly Asp Met Asn Pro Ala Asn			1920
625	630	635	640

tgg ccg cgc gaa cgc gcg tgg gcc ctc aag aat cct cac ctg gct tac Trp Pro Arg Glu Arg Ala Trp Ala Leu Lys Asn Pro His Leu Ala Tyr 645 650 655	1968
aat ccc ttc agg atg cct acg act tcc acg gct tct caa aac acc gtg Asn Pro Phe Arg Met Pro Thr Thr Ser Thr Ala Ser Gln Asn Thr Val 660 665 670	2016
tcc acc acc cct cgg agg ccg tcg act cca cgc gcc gcg gtg aca caa Ser Thr Thr Pro Arg Arg Pro Ser Thr Pro Arg Ala Ala Val Thr Gln 675 680 685	2064
aca gcg tct cgg gac gcc gct gat gag gtt tgg gct tta agg gac caa Thr Ala Ser Arg Asp Ala Ala Asp Glu Val Trp Ala Leu Arg Asp Gln 690 695 700	2112
act gca gag tca ccg gtc gaa gac agc gag gag gaa gac gac tcc Thr Ala Glu Ser Pro Val Glu Asp Ser Glu Glu Asp Asp Asp Ser 705 710 715 720	2160
tcg gac acc ggc tcc gtc gtc agc ctg gga cac aca aca ccg tcg tcc Ser Asp Thr Gly Ser Val Val Ser Leu Gly His Thr Thr Pro Ser Ser 725 730 735	2208
gat tac aac aac gac gtc att tcg cct ccc agt cag acg ccc gag cag Asp Tyr Asn Asn Asp Val Ile Ser Pro Pro Ser Gln Thr Pro Glu Gln 740 745 750	2256
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acg aca tcc acg agc cag aaa ccg gtg ctg ggc aag cga gtc gcg acg Thr Thr Ser Thr Ser Gln Lys Pro Val Leu Gly Lys Arg Val Ala Thr 770 775 780	2352
ccg cac gcg tcc gcc cga gcg cag acg gtg acg tcg acg ccg gtt cag Pro His Ala Ser Ala Arg Ala Gln Thr Val Thr Ser Thr Pro Val Gln 785 790 795 800	2400
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acg ctg ttg caa cct caa ccg gct tcg tct aaa acg acg tca tca agg Thr Leu Leu Gln Pro Gln Pro Ala Ser Ser Lys Thr Thr Ser Ser Arg 820 825 830	2496
aac gtg act tct ggc gcg gga acc tct tcc gct tct tcg gct cga cag Asn Val Thr Ser Gly Ala Gly Thr Ser Ser Ala Ser Ser Ala Arg Gln 835 840 845	2544
ccg tca gcc tcg gcg tcc gtt ttg tcg ccc acg gag gat gat gtc gtg Pro Ser Ala Ser Ala Ser Val Leu Ser Pro Thr Glu Asp Asp Val Val 850 855 860	2592

tcc ccc gcc aca tcg ccg ctg tcc atg ctt tcg tca gcc tct ccg tcc Ser Pro Ala Thr Ser Pro Leu Ser Met Leu Ser Ser Ala Ser Pro Ser 865	870	875	880	2640
ccg gcc aag agt gcc ccc ccg tct ccg gtg aaa ggc ccg ggc agc cgc Pro Ala Lys Ser Ala Pro Pro Ser Pro Val Lys Gly Arg Gly Ser Arg 885	890	895		2688
gtc ggt gtt cct tcc ttg aaa cct act ttg ggc ggc aag gcg gtg gta Val Gly Val Pro Ser Leu Lys Pro Thr Leu Gly Gly Lys Ala Val Val 900	905	910		2736
ggt cga ccg ccc tcg gtc ccc gtg agc ggt agc gcg ccg ggt cgc ctg Gly Arg Pro Pro Ser Val Pro Val Ser Gly Ser Ala Pro Gly Arg Leu 915	920	925		2784
tcc ggc agc agc cgg gcc tcg acc acg ccg acg tat ccc gcg gta Ser Gly Ser Ser Arg Ala Ala Ser Thr Thr Pro Thr Tyr Pro Ala Val 930	935	940		2832
acc acc gtt tac cca ccg tcg tct acg gcc aaa agc agc gta tcg aat Thr Thr Val Tyr Pro Pro Ser Ser Thr Ala Lys Ser Ser Val Ser Asn 945	950	955	960	2880
gcg ccg cct gtg gcc tcc ccc tcc atc ctg aaa ccg ggg gcg agc gcg Ala Pro Pro Val Ala Ser Pro Ser Ile Leu Lys Pro Gly Ala Ser Ala 965	970	975		2928
gct ttg caa tca cgc cgc tcg acg ggg acc gcc gcc gta ggt tcc ccc Ala Leu Gln Ser Arg Arg Ser Thr Gly Thr Ala Ala Val Gly Ser Pro 980	985	990		2976
gtc aag agc acg acg ggc atg aaa acg gtg gct ttc gac cta tcg tcg Val Lys Ser Thr Thr Gly Met Lys Thr Val Ala Phe Asp Leu Ser Ser 995	1000	1005		3024
ccc cag aag agc ggt acg ggg ccg caa ccg ggt tct gcc ggc atg ggg Pro Gln Lys Ser Gly Thr Gly Pro Gln Pro Gly Ser Ala Gly Met Gly 1010	1015	1020		3072
ggc gcc aaa acg ccg tcg gac gcc gtg cag aac atc ctc caa aag atc Gly Ala Lys Thr Pro Ser Asp Ala Val Gln Asn Ile Leu Gln Lys Ile 1025	1030	1035	1040	3120
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 Ala His Pro Lys Ile Leu Lys Lys Cys Gly Glu Lys Arg Leu His Arg  
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 Glu Leu Arg Phe His Asn Pro Asp Leu Ser Ser Val Leu Glu Glu Phe  
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 Glu Val Arg Cys Val Ala Val Ala Arg Arg Gly Tyr Thr Tyr Pro Phe  
 85 90 95  
 Gly Asp Arg Gly Lys Ala Arg Asp His Leu Ala Val Leu Asp Arg Thr  
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 Glu Phe Asp Thr Asp Val Arg His Asp Ala Glu Ile Val Glu Arg Ala  
 115 120 125  
 Leu Val Ser Ala Val Ile Leu Ala Lys Met Ser Val Arg Glu Thr Leu  
 130 135 140  
 Val Thr Ala Ile Gly Gln Thr Glu Pro Ile Ala Phe Val His Leu Lys  
 145 150 155 160  
 Asp Thr Glu Val Gln Arg Ile Glu Glu Asn Leu Glu Gly Val Arg Arg  
 165 170 175  
 Asn Met Phe Cys Val Lys Pro Leu Asp Leu Asn Leu Asp Arg His Ala  
 180 185 190  
 Asn Thr Ala Leu Val Asn Ala Val Asn Lys Leu Val Tyr Thr Gly Arg  
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 Leu Ile Met Asn Val Arg Arg Ser Trp Glu Glu Leu Glu Arg Lys Cys  
 210 215 220  
 Leu Ala Arg Ile Gln Glu Arg Cys Lys Leu Leu Val Lys Glu Leu Arg  
 225 230 235 240  
 Met Cys Leu Ser Phe Asp Ser Asn Tyr Cys Arg Asn Ile Leu Lys His  
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 Ala Val Glu Asn Gly Asp Ser Ala Asp Thr Leu Leu Glu Leu Leu Ile  
 260 265 270  
 Glu Asp Phe Asp Ile Tyr Val Asp Ser Phe Pro Gln Ser Ala His Thr  
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 Phe Leu Gly Ala Arg Ser Pro Ser Leu Glu Phe Asp Asp Asp Ala Asn  
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 His Val Pro Thr Gln Pro Leu Asp Gly Trp Ser Trp Ile Ala Ser Pro  
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 405 410 415  
 Pro Ser Ala Ser Arg Arg Leu Phe Gly Ser Ser Ala Asp Glu Asp Asp  
 420 425 430  
 Asp Asp Asp Asp Asp Glu Lys Asn Ile Phe Thr Pro Ile Lys Lys Pro  
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 Gly Thr Ser Gly Lys Gly Ala Ala Ser Gly Gly Val Ser Ser Ile  
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 Phe Ser Gly Leu Leu Ser Ser Gly Ser Gln Lys Pro Thr Ser Gly Pro

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Leu Asn Ile Pro Gln Gln Gln Gln Arg His Ala Ala Phe Ser	Leu Val		
485	490	495	
Ser Pro Gln Val Thr Lys Ala Ser Pro Gly Arg Val Arg Arg Asp Ser			
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Ala Trp Asp Val Arg Pro Leu Thr Glu Thr Arg Gly Asp Leu Phe Ser			
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Gly Asp Glu Asp Ser Asp Ser Ser Asp Gly Tyr Pro Pro Asn Arg Gln			
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Asp Pro Arg Phe Thr Asp Thr Leu Val Asp Ile Thr Asp Thr Glu Thr			
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Ile Leu Thr Pro Thr Pro Val Asn Pro Ser Thr Ala Pro Ala Pro Ala			
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Pro Thr Pro Thr Phe Ala Gly Thr Gln Thr Pro Val Asn Gly Asn Ser			
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Trp Pro Arg Glu Arg Ala Trp Ala Leu Lys Asn Pro His Leu Ala Tyr			
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Asn Pro Phe Arg Met Pro Thr Thr Ser Thr Ala Ser Gln Asn Thr Val			
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Ser Thr Thr Pro Arg Arg Pro Ser Thr Pro Arg Ala Ala Val Thr Gln			
675	680	685	
Thr Ala Ser Arg Asp Ala Ala Asp Glu Val Trp Ala Leu Arg Asp Gln			
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Thr Ala Glu Ser Pro Val Glu Asp Ser Glu Glu Glu Asp Asp Asp Ser			
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Ser Asp Thr Gly Ser Val Val Ser Leu Gly His Thr Thr Pro Ser Ser			
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Asp Tyr Asn Asn Asp Val Ile Ser Pro Pro Ser Gln Thr Pro Glu Gln			
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Pro His Ala Ser Ala Arg Ala Gln Thr Val Thr Ser Thr Pro Val Gln			
785	790	795	800
Gly Arg Leu Glu Lys Gln Val Ser Gly Thr Pro Ser Thr Val Pro Ala			
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Thr Leu Leu Gln Pro Gln Pro Ala Ser Ser Lys Thr Thr Ser Ser Arg			
820	825	830	
Asn Val Thr Ser Gly Ala Gly Thr Ser Ser Ala Ser Ser Ala Arg Gln			
835	840	845	
Pro Ser Ala Ser Ala Ser Val Leu Ser Pro Thr Glu Asp Asp Val Val			
850	855	860	
Ser Pro Ala Thr Ser Pro Leu Ser Met Leu Ser Ser Ala Ser Pro Ser			
865	870	875	880
Pro Ala Lys Ser Ala Pro Pro Ser Pro Val Lys Gly Arg Gly Ser Arg			
885	890	895	
Val Gly Val Pro Ser Leu Lys Pro Thr Leu Gly Gly Lys Ala Val Val			
900	905	910	
Gly Arg Pro Pro Ser Val Pro Val Ser Gly Ser Ala Pro Gly Arg Leu			
915	920	925	

Ser Gly Ser Ser Arg Ala Ala Ser Thr Thr Pro Thr Tyr Pro Ala Val  
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Thr Thr Val Tyr Pro Pro Ser Ser Thr Ala Lys Ser Ser Val Ser Asn  
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Ala Leu Gln Ser Arg Arg Ser Thr Gly Thr Ala Ala Val Gly Ser Pro  
980 985 990  
Val Lys Ser Thr Thr Gly Met Lys Thr Val Ala Phe Asp Leu Ser Ser  
995 1000 1005  
Pro Gln Lys Ser Gly Thr Gly Pro Gln Pro Gly Ser Ala Gly Met Gly  
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